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OM protein - protein search, using sw model

Run on: November 1, 2001, 16:24:05 ; Search time 12.69 seconds  
(without alignments)  
196.837 Million cell updates/sec

Title: US-09-652-345-6

Perfect score: 543

Sequence: 1 ILLVSDDEHRAAQRLET.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued\_Patents\_AA:\*
- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	540	99.4	920	1	US-08-026-138E-9
2	540	99.4	920	1	US-08-026-138E-10
3	538	99.1	922	2	US-08-231-193A-14
4	538	99.1	922	2	US-08-231-193A-20
5	538	99.1	922	2	US-08-486-273A-14
6	538	99.1	922	2	US-08-486-273A-20
7	538	99.1	922	3	US-08-480-474-14
8	538	99.1	922	3	US-08-480-474-20
9	538	99.1	922	3	US-08-940-086A-14
10	538	99.1	922	3	US-08-940-086A-20
11	538	99.1	938	2	US-08-231-193A-2
12	538	99.1	938	2	US-08-486-273A-2
13	538	99.1	938	3	US-08-480-474-2
14	538	99.1	938	3	US-08-940-086A-2
15	538	99.1	976	2	US-08-231-193A-22
16	538	99.1	976	2	US-08-486-273A-22
17	538	99.1	976	3	US-08-480-474-22
18	538	99.1	976	3	US-08-940-086A-22
19	532	98.0	863	4	US-08-436-332B-2
20	517.5	95.3	943	2	US-08-231-193A-36
21	517.5	95.3	943	2	US-08-486-273A-36
22	517.5	95.3	943	3	US-08-480-474-36
23	517.5	95.3	943	3	US-08-940-086A-36
24	517.5	95.3	959	2	US-08-231-193A-24
25	517.5	95.3	959	2	US-08-486-273A-24
26	517.5	95.3	959	3	US-08-480-474-24
27	517.5	95.3	959	3	US-08-940-086A-24

28	517.5	95.3	997	2	US-08-231-193A-38	Sequence 38, Appl
29	517.5	95.3	997	2	US-08-486-273A-38	Sequence 38, Appl
30	517.5	95.3	997	2	US-08-480-474-38	Sequence 38, Appl
31	517.5	95.3	997	2	US-08-940-086A-38	Sequence 38, Appl
32	400	73.7	854	2	US-08-231-193A-32	Sequence 32, Appl
33	400	73.7	854	2	US-08-486-273A-32	Sequence 32, Appl
34	400	73.7	854	2	US-08-480-474-32	Sequence 32, Appl
35	400	73.7	854	2	US-08-940-086A-32	Sequence 32, Appl
36	400	73.7	870	2	US-08-231-193A-30	Sequence 30, Appl
37	400	73.7	870	2	US-08-486-273A-30	Sequence 30, Appl
38	400	73.7	870	2	US-08-480-474-30	Sequence 30, Appl
39	400	73.7	870	2	US-08-940-086A-30	Sequence 30, Appl
40	400	73.7	908	2	US-08-231-193A-34	Sequence 34, Appl
41	400	73.7	908	2	US-08-486-273A-34	Sequence 34, Appl
42	400	73.7	908	2	US-08-480-474-34	Sequence 34, Appl
43	400	73.7	908	2	US-08-940-086A-34	Sequence 34, Appl
44	379.5	69.9	777	2	US-08-231-193A-16	Sequence 16, Appl
45	379.5	69.9	777	2	US-08-486-273A-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-08-026-138E-9  
; Sequence 9, Application US/08026138E  
; Patent No. 5502166  
; GENERAL INFORMATION:  
; APPLICANT: Masayoshi MISHINA  
; TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nishiohata Residence 1-107  
; STREET: 5214, Nishiohata-machi  
; CITY: Niigata-shi  
; STATE: Niigata-ken  
; COUNTRY: JAPAN  
; ZIP: 951  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS V.5  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/026,138E  
; FILING DATE: 26-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 39563/1992  
; FILING DATE: 26-FEB-1992  
; APPLICATION NUMBER: JP 173155/1992  
; FILING DATE: 30-JUN-1992  
; APPLICATION NUMBER: JP 215017/1992  
; FILING DATE: 12-AUG-1992  
; APPLICATION NUMBER: JP 303878/1992  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hamburg, C.Bruce  
; REGISTRATION NUMBER: 22,389  
; REFERENCE/DOCKET NUMBER: F-4551  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 986-2340  
; TELEFAX: (212) 953-7733  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 920 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single strand  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: mouse  
; TISSUE TYPE: brain  
; PUBLICATION INFORMATION:

US-08-026-138E-10

[illegible]

Db 223 ASEDATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

## RESULT 4

US-08-231-193A-20  
; Sequence 20, Application US/08231193A  
; Patent No. 5849895

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen W.

APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR

TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: U.S.A.

ZIP: 92101-2926

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/231,193A

FILING DATE: 20-APR-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/052,459

FILING DATE: 20-APR-1993

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 922 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-231-193A-20

## Query Match

Best Local Similarity 99.1%; Score 538; DB 2; Length 922;

Mismatches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 60

Db 163 IILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 222

Qy 61 ASEDATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 223 ASEDATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

## RESULT 5

US-08-486-273A-14  
; Sequence 14, Application US/08486273A  
; Patent No. 5985586

## GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie P.

APPLICANT: Ellis, Steven B.

APPLICANT: Liaw, Chen W.

APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA

TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: U.S.A.

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,273A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/231,193

FILING DATE: 20-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9383B

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 922 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-486-273A-14

## Query Match

Best Local Similarity 99.1%; Score 538; DB 2; Length 922;

Mismatches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 60

Db 163 IILLVSDHGGRAAKRLETLLEERESKAQKVLQFDGPKNTVALLMEARELEAVIILS 222

Qy 61 ASEDATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 223 ASEDATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

## RESULT 6

US-08-486-273A-20

; Sequence 20, Application US/08486273A

; Patent No. 5985586

; GENERAL INFORMATION:

; APPLICANT: Daggett, Lorrie P.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lu, Chin-Chun

; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA

; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92101-2926

; COMPUTER READABLE FORM: disk

; MEDIUM TYPE: Floppy disk



Db 163 IILLVSDDEGAAKRLTLEERESKAEKVLQDFGPKNTVNTALLMEARELEAVIILS 222  
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111  
Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

## RESULT 9

US-08-940-086A-14  
; Sequence 14, Application US/08940086A  
; Patent No. 6111091  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie P.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lu, Chin-Chun  
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Heller Ehrman White & McAuliffe  
; STREET: 4250 Executive Square, 7th Floor  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940.086A  
; FILING DATE: 29-SEPT-97  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/231,193  
; FILING DATE: 20-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/052,449  
; FILING DATE: 20-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 24735-9383C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 450-8499  
; TELEFAX: (619) 450-8499  
; INFORMATION FOR SEQ ID NO: 14:  
; LENGTH: 922 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-940-086A-14

Query Match 99.1%; Score 538; DB 3; Length 922;  
Best Local Similarity 98.2%; Pred. No. 5.9e-57;  
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDDEGAAKRLTLEERESKAEKVLQDFGPKNTVNTALLMEARELEAVIILS 60  
Db 163 IILLVSDDEGAAKRLTLEERESKAEKVLQDFGPKNTVNTALLMEARELEAVIILS 222  
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111  
Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

## RESULT 10

US-08-940-086A-20

; Sequence 20, Application US/08940086A  
; Patent No. 6111091  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie P.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lu, Chin-Chun  
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Heller Ehrman White & McAuliffe  
; STREET: 4250 Executive Square, 7th Floor  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/940.086A  
; FILING DATE: 29-SEPT-97  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/231,193  
; FILING DATE: 20-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/052,449  
; FILING DATE: 20-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 24735-9383C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 450-8499  
; TELEFAX: (619) 450-8499  
; INFORMATION FOR SEQ ID NO: 20:  
; LENGTH: 922 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-940-086A-20

Query Match 99.1%; Score 538; DB 3; Length 922;  
Best Local Similarity 98.2%; Pred. No. 5.9e-57;  
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDDEGAAKRLTLEERESKAEKVLQDFGPKNTVNTALLMEARELEAVIILS 60  
Db 163 IILLVSDDEGAAKRLTLEERESKAEKVLQDFGPKNTVNTALLMEARELEAVIILS 222  
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111  
Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

## RESULT 11

US-08-231-193A-2  
; Sequence 2, Application US/08231193A  
; Patent No. 5849895  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie P.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lu, Chin-Chun  
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
; NUMBER OF SEQUENCES: 63

Qy	1	IILVSDHDEHGRAAKRLETLLEERSKAEKVLFQDPGTKNVTALLMEARELEARVILLS	60
Db	163	IILVSDHDEHGRAAKRLETLLEERSKAEKVLFQDPGTKNVTALLMEARELEARVILLS	222
Qy	61	ASEDDAATVYRAAAMLNMTSGYVWLVGEREISGNALRYAPDGIIGIQLIN	111
Db	223	ASEDDAATVYRAAAMLNMTSGYVWLVGEREISGNALRYAPDGIIGIQLIN	273

RESULT 13  
US-08-480-474-2  
; Sequence 2, Application US/08480474  
; Patent No. 6033865

sequence 2, Application# US/06480474  
Patent No. 6033865  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
TITLE OF INVENTION: SAME AND USEFUL  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:

RESULT 12  
US-08-486-273A-2  
; Sequence 2, Application US/08486273A  
; Patent No. 5985586

COUNTRY: U.S.A.  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,474  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9382B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEO ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 938 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-480-474-2

Query Match 99.1%; Score 538; DB 3; Length 938;  
Best Local Similarity 98.2%; Pred. No. 6.1e-57;  
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPTKNTALLMEARELEAVIILS 60  
Db 163 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPTKNTALLMEARELEAVIILS 222  
Qy 61 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
Db 223 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 14  
US-08-940-086A-2  
Sequence 2, Application US/08940086A  
Patent No. 6111091  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McAuliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940.086A  
FILING DATE: 29-SEPT-97  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/231.193  
FILING DATE: 20-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/052.449  
FILING DATE: 20-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24735-9383C  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 450-8499  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 938 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-940-086A-2

Query Match 99.1%; Score 538; DB 3; Length 938;  
Best Local Similarity 98.2%; Pred. No. 6.1e-57;

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPTKNTALLMEARELEAVIILS 60  
Db 163 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPTKNTALLMEARELEAVIILS 222  
Qy 61 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
Db 223 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 15  
US-08-231-193A-22  
Sequence 22, Application US/08231193A  
Patent No. 5849895  
GENERAL INFORMATION:  
APPLICANT: Daggett, Lorrie P.  
APPLICANT: Ellis, Steven B.  
APPLICANT: Liaw, Chen W.  
APPLICANT: Lu, Chin-Chun  
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,193A  
FILING DATE: 20-APR-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/052,459  
FILING DATE: 20-APR-1993  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 6362-9383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-238-0999  
TELEFAX: 619-238-0062  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 976 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-231-193A-22

Query Match 99.1%; Score 538; DB 2; Length 976;  
Best Local Similarity 98.2%; Pred. No. 6.4e-57;  
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPTKNTALLMEARELEAVIILS 60  
Db 163 IILLVSDHDEGAAKRLTLLERESKAEKVLQFDGPTKNTALLMEARELEAVIILS 222  
Qy 61 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
Db 223 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: November 1, 2001, 16:24:05 ; Search time 21.33 Seconds  
(without alignments)  
315.483 Million cell updates/sec

Title: US-09-652-345-6  
Perfect score: 543  
Sequence: 1 IILLVSDHGGRAAQRRLT.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Minimum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
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19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	100.0	111	22 AAB74434	Human NMDA recepto
2	540	99.4	920	15 AAR49043	NMDA receptor chan
3	540	99.4	920	15 AAR49044	NMDA receptor chan
4	538	99.1	885	15 AAR57328	NMDAR1-1. Homo sa
5	538	99.1	885	16 AAR80973	Human excitatory a
6	538	99.1	918	15 AAR66042	Human N-methyl-D-a
7	538	99.1	922	15 AAR66046	Human NMDA recepto
8	538	99.1	922	15 AAR66043	Human N-methyl-D-a
9	538	99.1	922	20 AAR85580	Human N-methyl-D-a
10	538	99.1	922	20 AAR85577	Human N-methyl-D-a
11	538	99.1	922	21 AAB26216	Human N-methyl-D-a

12	538	99.1	922	21	AAB26219	Human N-methyl-D-a
13	538	99.1	922	21	AAV56114	Human N-methyl-D-a
14	538	99.1	922	21	AAV56117	Human N-methyl-D-a
15	538	99.1	938	15	AAR66035	Human N-methyl-D-a
16	538	99.1	938	15	AAR85572	Human N-methyl-D-a
17	538	99.1	938	21	AAB26211	Human N-methyl-D-a
18	538	99.1	938	21	AAV56109	Human N-methyl-D-a
19	538	99.1	976	15	AAR66047	Human NMDA recepto
20	538	99.1	976	20	AAR85581	Human N-methyl-D-a
21	538	99.1	976	21	AAB26220	Human N-methyl-D-a
22	538	99.1	976	21	AAV56118	Human N-methyl-D-a
23	532	98.0	885	15	AAV55530	Human NMDA Rle rec
24	532	98.0	922	15	AAV55531	Human NMDA Rle rec
25	532	98.0	938	15	AAV55532	Human NMDA Rle rec
26	517.5	95.3	943	15	AAR66054	Human NMDA recepto
27	517.5	95.3	943	15	AAR85588	Human N-methyl-D-a
28	517.5	95.3	943	21	AAB26227	Human N-methyl-D-a
29	517.5	95.3	943	21	AAV56123	Human NMDAR1-163-d
30	517.5	95.3	959	15	AAR66048	Human NMDA recepto
31	517.5	95.3	959	20	AAR85582	Human N-methyl-D-a
32	517.5	95.3	959	21	AAB26221	Human N-methyl-D-a
33	517.5	95.3	959	21	AAV56119	Human N-methyl-D-a
34	517.5	95.3	997	15	AAR66055	Human NMDA recepto
35	517.5	95.3	997	20	AAR85589	Human N-methyl-D-a
36	517.5	95.3	997	21	AAB26228	Human N-methyl-D-a
37	517.5	95.3	997	21	AAV56126	Human NMDAR1-163-d
38	513	94.5	111	22	AAB74435	Human NMDA recepto
39	400	73.7	854	15	AAR66052	Human NMDA recepto
40	400	73.7	854	20	AAR85586	Human N-methyl-D-a
41	400	73.7	854	21	AAB26225	Human N-methyl-D-a
42	400	73.7	854	21	AAV56123	Human NMDAR1-delta
43	400	73.7	870	15	AAR66051	Human NMDA recepto
44	400	73.7	870	20	AAR85585	Human N-methyl-D-a
45	400	73.7	870	21	AAB26224	Human N-methyl-D-a

ALIGNMENTS

RESULT 1  
AAB74434  
ID AAB74434 standard; protein; 111 AA.  
XX AC AAB74434;  
XX DT 29-MAY-2001 (first entry)  
XX DE Human NMDA receptor NR1011 subunit.  
XX KW Human; NMDA receptor; CNS; N-methyl-D-aspartate receptor; modulator;  
KW neuropathic pain; drug dependency; epilepsy; glaucoma;  
KW neurodegenerative disease; amyotrophic lateral sclerosis; anxiety;  
KW brain cell death; ischaemia; stroke; trauma.  
XX OS Homo sapiens.  
XX PN WO200116601-A1.  
XX PD 08-MAR-2001.  
XX PF 31-AUG-2000; 2000WO-US23985.  
XX PR 31-AUG-1999; 99US-0151802.  
XX PA (UYBO-) UNIV BOSTON.  
XX PI Farb DH, Russek S, Jang M, Gibbs T;  
XX PR WPI; 2001-257712/26.  
XX PT Identifying a subunit specific modulator of the NMDA receptor for  
PT treating diseases such as neurodegenerative diseases, and ischemia  
PT comprises assaying for an increase or decrease in receptor activity in



PT the presence of the modulator -

XX \*

PS Example 5; Fig 23; 135pp; English.

XX

CC The present invention describes a method of identifying subunit specific

CC modulators of the N-methyl-D-aspartate (NMDA) receptor, involving

CC contacting a number of different receptors with a neurotransmitter

CC recognition site in the presence of the agent of interest, and assaying

CC for receptor activity. Modulators of this type are useful in the

CC treatment of neuropathic pain, drug withdrawal and dependency, epilepsy,

CC glaucoma, chronic neurodegenerative diseases, amyotrophic lateral

CC sclerosis, anxiety disorders, brain cell death, ischaemia, stroke and

XX trauma.

XX

SQ Sequence 111 AA;

Query Match 100.0%; Score 543; DB 22; Length 111;

Best Local Similarity 100.0%; Pred. No. 2.9e-58;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDPGTKNVTALLMEARELEARVILS 60

Db 1 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDPGTKNVTALLMEARELEARVILS 60

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 61 asddaatvyraaamlnmtgsgyvwlvgereisgnalryapdgiigqlin 111

RESULT 2

AAR49043

ID AAR49043 standard; Protein; 920 AA.

XX

AC AAR49043;

XX

DT 20-SEP-1994 (first entry)

XX

DE NMDA receptor channel subunit zeta-1-N598Q.

XX

KW NMDA; N-methyl-D-aspartate; receptor; channel; subunit;

KW brain; cerebellum; neurotransmission; synapse; memory;

KW learning; neurocyte; necrosis; cerebral ischemia;

KW status epilepticus; CNS; central nervous system.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Misc-difference 598 /note= "N598Q"

FT

XX

PN WO9404698-A.

XX

PD 03-MAR-1994.

XX

PF 12-AUG-1993; 93WO-JP01143.

XX

PR 12-AUG-1992; 92JP-0215017.

XX

PA (MITU ) MITSUBISHI KASEI CORP.

XX

PI Mishina M;

XX

DR WPI; 1994-083212/10.

DR N-PSDB; AAQ55980.

XX

XX NMDA receptor channel epsilon and zeta sub-unit proteins -

PT obtained by Xenopus oocyte expression of modified receptor mRNA

XX

PS Claim 1; Page 21-27; 44pp; Japanese.

XX

XX NMDA receptor cDNA from a mouse cerebellum-derived library

CC is subjected to site-specific mutagenesis to give cDNA coding

CC

CC for the desired modified proteins, mRNA derived from this

CC is then expressed in Xenopus laevis oocytes.

CC The modified NMDA receptor channel proteins (AAQ55979-81)

CC are useful as tools for investigation of the mechanism of

CC neurotransmission across synapses, the development of synapse

CC plasticity (basic to memory and learning), the development of

CC neurocyte necrosis as a result of disorders such as cerebral

CC ischemia and status epilepticus. This is necessary for understanding

CC the mechanisms of neurotransmission in the CNS and the organisation

CC and pathology of the brain, and in the development of drugs and

CC therapy for brain diseases and genetically determined disorders.

XX

SQ Sequence 920 AA;

Query Match 99.4%; Score 540; DB 15; Length 920;

Best Local Similarity 99.1%; Pred. No. 1.4e-56;

Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDPGTKNVTALLMEARELEARVILS 60

Db 145 IILLVSDHDEGRAQKRLTLLERESKAQKVLQFDPGTKNVTALLMEARELEARVILS 204

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111

Db 205 asddaatvyraaamlnmtgsgyvwlvgereisgnalryapdgiigqlin 255

RESULT 3

AAR49044

ID AAR49044 standard; Protein; 920 AA.

XX

AC AAR49044;

XX

DT 20-SEP-1994 (first entry)

XX

DE NMDA receptor channel subunit zeta-1-ZAZ.

XX

KW NMDA; N-methyl-D-aspartate; receptor; channel; subunit;

KW brain; cerebellum; neurotransmission; synapse; memory;

KW learning; neurocyte; necrosis; cerebral ischemia;

KW status epilepticus; CNS; central nervous system.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Misc-difference 576..581 /note= "mouse-derived sequence altered

FT to TSDQN"

XX

PN WO9404698-A.

XX

PD 03-MAR-1994.

XX

PF 12-AUG-1993; 93WO-JP01143.

XX

PR 12-AUG-1992; 92JP-0215017.

XX

PA (MITU ) MITSUBISHI KASEI CORP.

XX

PI Mishina M;

XX

DR WPI; 1994-083212/10.

DR N-PSDB; AAQ55981.

XX

XX NMDA receptor channel epsilon and zeta sub-unit proteins -

PT obtained by Xenopus oocyte expression of modified receptor mRNA

XX

PS Claim 1; Page 27-33; 44pp; Japanese.

XX

XX NMDA receptor cDNA from a mouse cerebellum-derived library

CC is subjected to site-specific mutagenesis to give cDNA coding

CC for the desired modified proteins. mRNA derived from this

CC



DR N-PSDB; AAQ79384.  
XX  
PT Isolated DNA encoding a human N-methyl-D-aspartate receptor

```

PI Daggett LP, Ellis SB, Liaw CW, Lu C;
XX WPI: 1994-341863/42.
DR N-PSDB; AAQ79388.
XX
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor
PT subunit - used as probes in the identification and isolation of
PT nucleic acids encoding related receptor subunits.
XX
XX Claim 5; Page 91-95; 156pp; English.
PS
XX The amino acid sequence of the novel N-methyl-D-aspartate (NMDA)
CC receptor 1A (NMDAR1A) clone NMDAR1-delta363 (sequence not given in the
CC specification). The clone contains a deletion of 121 a.a. between
CC a.a. 900-938 of the NMDAR1A sequence (AAQ79370). The clone uses an
CC alternative stop codon at bases 3391-3 of the NMDAR1A sequence. This
CC produces an alternative 22 a.a. at the C-terminus of this clone. This
CC variant clone was constructed, by recombination, using the clones:
CC NMDA10 (AAQ79384), NMDA11 (AAQ79385), NMDA7 (AAQ79386) and NMDA3
CC (AAQ79387). These clones were used to construct a series of variants
CC (AAQ79388-98) of the NMDAR1A receptor gene. The NMDAR1A gene isolated
CC from a cDNA library derived from human hippocampal tissue RNA using
CC probes corresponding to sequences in the rat NMDAR1A receptor DNA. The
CC 2.1 kb EcoRI-HindIII fragment from clone NMDA11, containing the 5',
CC portion of the gene, with the 3.3 kb BglII-EcoRI fragment of clone
CC NMDA10, containing the 3' portion of the gene, were ligated to generate
CC the full length sequence (AAQ79370) of the NMDAR1A gene in plasmid
CC pCDNA1. The resultant clone, NMDAR1A, contains tcc 261 bp of 5'
CC untranslated DNA, the entire coding region for the NMDAR1A receptor and
CC 1220 bp of 3' untranslated DNA. The NMDA receptor contains a second
CC subunit selected from the subunits 2A (AAQ79375), 2B (AAQ79377), 2C
CC (AAQ79372) and 2D (AAQ79378). The receptor forms part of a family of NMDA
CC receptors which have cation-selective channels and bind glutamate and
CC NMDA. The expression of the genes allows the reconstruction of the NMDA
CC receptor. The complete receptor can be used to identify compounds which
CC bind or are antagonistic to the human NMDA receptor.
XX
XX Sequence 922 AA;
SQ
Query Match 99.1%; Score 538; DB 15; Length 922;
Best Local Similarity 98.2%; Pred. No. 2.5e-56;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTVNTALLMEARELEAVIILS 60
DB 163 IILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTVNTALLMEARELEAVIILS 222
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
DB 223 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273
RESULT 8
AAQ66043
ID AAR66043 standard; Protein; 922 AA.
XX
XX AAR66043;
XX
XX 03-JUL-1995 (first entry)
XX
XX Human N-methyl-D-aspartate receptor subunit 1A a.a. seq.clone NMDA11.
XX N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;
XX glutamate; hippocampus; rat; pCDNA1; NMDA receptor; antagonist.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 900..901
XX /note= "38 a.a. deletion of the C-terminal NMDAR1A a.a.
XX sequence between these residues"
XX

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```

PN WO9424284-A.
XX
XX 27-OCT-1994.
XX
XX 20-APR-1994; 94WO-US04387.
XX
XX 20-APR-1993; 93US-0052449.
XX
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
PA
XX Daggett LP, Ellis SB, Liaw CW, Lu C;
PI
XX WPI: 1994-341863/42.
DR N-PSDB; AAQ79385.
XX
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor
PT subunit - used as probes in the identification and isolation of
PT nucleic acids encoding related receptor subunits.
XX
XX Claim 5; Page 91-95; 156pp; English.
PS
XX The amino acid sequence of the novel N-methyl-D-aspartate (NMDA)
CC receptor 1A (NMDAR1A) from clone NMDA11 (sequence not given in the
CC specification). The clone contains a deletion of the residues 901-938 of
CC the NMDAR1A sequence (AAR66035). The clone uses the next in-frame stop
CC codon at pos. 3391-3 of the NMDAR1A DNA sequence (AAQ79370). This
CC encodes an alternative 22 a.a. at the C-terminus of the protein. This
CC clone was one of 8 isolated from a cDNA library derived from human
CC hippocampal tissue RNA using probes corresponding to sequences in the rat
CC NMDAR1A receptor DNA. The 2.1 kb EcoRI-HindIII fragment from clone NMDA11
CC containing the 5' portion of the gene, with the 3.3 kb BglII-EcoRI
CC fragment of clone NMDA10 (AAQ79384), containing the 3' portion of the
CC gene, were ligated to generate the full length sequence (AAQ79370) of the
CC NMDAR1A gene in plasmid pCDNA1. The entire coding region for the NMDAR1A
CC receptor and 1220 bp of 3' untranslated DNA. The NMDA receptor contains
CC a second subunit selected from the subunits 2A (AAQ79375), 2B (AAQ79377),
CC 2C (AAQ79372) and 2D (AAQ79378). The receptor forms part of a family of
CC NMDA receptors which have cation-selective channels and bind glutamate
CC and NMDA. Based on the sequences of clones: NMDA10, NMDA11, NMDA7
CC (AAQ79386) and NMDA3 (AAQ79387), a series of variants (AAQ79388-98) of
CC the NMDAR1A receptor gene were constructed. The expression of the genes
CC allows the reconstruction of the NMDA receptor. The complete receptor
CC can be used to identify compounds which bind or are antagonistic to the
CC human NMDA receptor.
XX
XX Sequence 922 AA;
SQ
Query Match 99.1%; Score 538; DB 15; Length 922;
Best Local Similarity 98.2%; Pred. No. 2.5e-56;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTVNTALLMEARELEAVIILS 60
DB 163 IILLVSDHDEGRAAKRLTLLERESKAELVQDPGKNTVNTALLMEARELEAVIILS 222
QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
DB 223 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273
RESULT 9
AAW85580
ID AAW85580 standard; Protein; 922 AA.
XX
XX AAW85580;
XX
XX 23-FEB-1999 (first entry)
XX
XX Human N-methyl-D-aspartate receptor subunit NMDAR1-delta363.
XX Human; N-methyl-D-aspartate receptor; NMDAR1;

```

KW NMDA-activated cation-selective ion channel; glutamate receptor.

XX Homo sapiens.

PN US5849895-A.

XX 15-DEC-1998.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1993; 93US-0052449.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

PA Daggett LP, Lu C;

PI WPI; 1999-069812/06.

DR N-PSDB; AAV82897.

XX DNA encoding N-methyl-D-aspartate receptor subunit - useful for the

PT assembly of functional glutamate receptor subunits

XX Disclosure; Columns 123-128; 203pp; English.

XX The present sequence represents a human N-methyl-D-aspartate (NMDA)

CC receptor (NMDAR) subunit, designated NMDAR1-delta363. The nucleic

CC acid sequence does not contain the 363 nucleotides 2962-3324, as set

CC forth in AAV82887. The NMDAR subunits contribute to the formation

CC of NMDA-activated cation-selective ion channels. In addition

CC to being useful for the production of NMDA receptor subunit proteins,

CC the nucleic acids are also useful as probes to identify and isolate

CC nucleic acids encoding related receptor subunits. Functional glutamate

CC receptors can be assembled from several NMDA receptor subunit proteins

CC of one type (homomeric) or from combinations of subunit proteins of

CC different types (heteromeric). The present invention also comprises

CC methods for using such receptor subunits to identify and characterise

CC compounds which affect the function of such receptors, e.g. agonists,

CC antagonists and modulators of glutamate receptor function. The invention

CC also comprises methods for determining whether unknown protein(s) are

CC functional as NMDA receptor subunits.

XX Sequence 922 AA;

XX Query Match 99.1%; Score 538; DB 20; Length 922;

XX Best Local Similarity 98.2%; Pred. No. 2.5e-56;

XX Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTALLMEARELEARVILS 60

Db 163 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTALLMEARELEARVILS 222

QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111

Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 10

AAW85577

ID AAW85577 standard; Protein; 922 AA.

XX AAW85577;

XX 23-FEB-1999 (first entry)

XX Human N-methyl-D-aspartate receptor subunit.

XX Human; N-methyl-D-aspartate receptor; NMDAR1;

XX NMDA-activated cation-selective ion channel; glutamate receptor.

XX Homo sapiens.

PN US5849895-A.

XX 15-DEC-1998.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1994; 94US-0231193.

XX 20-APR-1993; 93US-0052449.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

PA Daggett LP, Lu C;

PI WPI; 1999-069812/06.

DR N-PSDB; AAV82894.

XX DNA encoding N-methyl-D-aspartate receptor subunit - useful for the

PT assembly of functional glutamate receptor subunits

XX Example 1; Columns 97-104; 203pp; English.

XX The present sequence represents a human N-methyl-D-aspartate (NMDA)

CC receptor subunit (NMDAR1). The nucleic acid sequence does not contain

CC the 363 nucleotides 2962-3324 or the 781 terminal 3' nucleotides,

CC as set forth in AAV82887. The cDNA sequence is derived from clone

CC NMDA11. The NMDAR subunits contribute to the formation of NMDA-activated

CC cation-selective ion channels. In addition to being useful for the

CC production of NMDA receptor subunit proteins, the nucleic acids are

CC also useful as probes to identify and isolate nucleic acids encoding

CC related receptor subunits. Functional glutamate receptors can be

CC assembled from several NMDA receptor subunit proteins of one type

CC (homomeric) or from combinations of subunit proteins of different

CC types (heteromeric). The present invention also comprises methods

CC for using such receptor subunits to identify and characterise

CC compounds which affect the function of such receptors, e.g. agonists,

CC antagonists and modulators of glutamate receptor function. The invention

CC also comprises methods for determining whether unknown protein(s) are

CC functional as NMDA receptor subunits.

XX Sequence 922 AA;

XX Query Match 99.1%; Score 538; DB 20; Length 922;

XX Best Local Similarity 98.2%; Pred. No. 2.5e-56;

XX Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTALLMEARELEARVILS 60

Db 163 ILLVSDHDEGRAAKRLTLLERESKAERVLQDPGKNTALLMEARELEARVILS 222

QY 61 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111

Db 223 ASDDAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 11

AAAB26216

ID AAAB26216 standard; Protein; 922 AA.

XX AAAB26216;

XX 23-FEB-2001 (first entry)

XX Human N-methyl-D-aspartate receptor subunit NMDAR1A #2.

XX Human; N-methyl-D-aspartate receptor; NMDA; NMDAR1A; ionotropic;

XX glutamate receptor; drug screening; animal model; disease diagnosis;

XX genetic screening.

XX Homo sapiens.

XX US6111091-A.



CC A method has been developed for identifying modulators of human  
 CC N-methyl-D-aspartate (NMDA) receptors. The method may be used for  
 CC identifying modulators of human NMDA receptors. The modulators may  
 CC be useful in controlling a wide range of neuronal processes including  
 CC fast excitatory synaptic transmission, regulation of neurotransmitter  
 CC releases, long-term potentiation, learning and memory, developmental  
 CC synaptic plasticity, hypoxic-ischaemic damage and neuronal cell death,  
 CC epileptiform seizures and the pathology of several neurodegenerative  
 CC disorders. AA238701 to AA238736, and AA56109 to AA56135 represent  
 CC sequences used in the exemplification of the present invention.

XX SQ Sequence 922 AA;

Query Match 99.1%; Score 538; DB 21; Length 922;

Best Local Similarity 98.2%; Pred. No. 2.5e-56;

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHGEGRRAAKRLETLLEERESKAQVLPDGTGNVNTALLMEARELEAVIILS 60  
 |||||  
 Db 163 IILLVSDHGEGRRAAKRLETLLEERESKAQVLPDGTGNVNTALLMEARELEAVIILS 222

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
 |||||  
 Db 223 aseddaatvyraraamlnmtgsgyvwlvgeresgnalryapdgiilgqlin 273

#### RESULT 14

AA56117

AA56117 standard; Protein; 922 AA.

XX AC AA56117;

XX DT 08-FEB-2000 (first entry)

XX DE Human N-methyl-D-aspartate receptor 1 subunit SEQ ID NO:20.

XX KW Human; N-methyl-D-aspartic acid; N-methyl-D-aspartic acid receptor;  
 KW NMDA; NMDAR; receptor subunit; cation-selective channel; modulator;  
 KW glutamate binding; glutamate receptor; NMDA receptor subunit;  
 KW neuronal processes; fast excitatory synaptic transmission; regulation;  
 KW neurotransmitter release; long-term potentiation; learning; memory;  
 KW developmental synaptic plasticity; hypoxic-ischaemic damage;  
 KW neuronal cell death; epileptiform seizure; neurodegenerative disorder.

XX OS Homo sapiens.

XX PN US985586-A.

XX PD 16-NOV-1999.

XX PF 06-JUN-1995; 95US-0486273.

XX PR 20-APR-1994; 94US-0231193.

XX PS 20-APR-1993; 93US-0052449.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Daggett LP, Ellis SB, Liaw CW;

XX XX WPI; 2000-022277/02.

XX DR N-PSDB; AA238711.

XX PT Identifying modulators of human N-methyl-D-aspartate receptors -

XX PS Claim 4; Column 123-128; 202pp; English.

XX CC A method has been developed for identifying modulators of human  
 CC N-methyl-D-aspartate (NMDA) receptors. The method may be used for  
 CC identifying modulators of human NMDA receptors. The modulators may  
 CC be useful in controlling a wide range of neuronal processes including  
 CC fast excitatory synaptic transmission, regulation of neurotransmitter  
 CC releases, long-term potentiation, learning and memory, developmental

CC synaptic plasticity, hypoxic-ischaemic damage and neuronal cell death,  
 CC epileptiform seizures and the pathology of several neurodegenerative  
 CC disorders. AA238701 to AA238736, and AA56109 to AA56135 represent  
 CC sequences used in the exemplification of the present invention.

XX SQ Sequence 922 AA;

Query Match 99.1%; Score 538; DB 21; Length 922;

Best Local Similarity 98.2%; Pred. No. 2.5e-56;

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IILLVSDHGEGRRAAKRLETLLEERESKAQVLPDGTGNVNTALLMEARELEAVIILS 60  
 |||||  
 Db 163 IILLVSDHGEGRRAAKRLETLLEERESKAQVLPDGTGNVNTALLMEARELEAVIILS 222

Qy 61 ASDDAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
 |||||  
 Db 223 aseddaatvyraraamlnmtgsgyvwlvgeresgnalryapdgiilgqlin 273

#### RESULT 15

AA66035

ID AAR66035 standard; Protein; 938 AA.

XX AC AAR66035;

XX DT 03-JUL-1995 (first entry)

XX DE Human N-methyl-D-aspartate receptor subunit 1A.

XX KW N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;  
 KW glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist.

XX OS Homo sapiens.

XX PN WO9424284-A.

XX PD 27-OCT-1994.

XX PF 20-APR-1994; 94WO-US04387.

XX PR 20-APR-1993; 93US-0052449.

XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX PI Daggett LP, Ellis SB, Liaw CW, Lu C;

XX DR WPI; 1994-341863/42.

XX DR N-PSDB; AAQ79370.

XX PT Isolated DNA encoding a human N-methyl-D-aspartate receptor  
 XX subunit - used as probes in the identification and isolation of  
 XX nucleic acids encoding related receptor subunits.

XX PS Claim 3; Page 91-95; 156pp; English.

XX CC The amino acid sequence of the novel N-methyl-D-aspartate (NMDA)  
 XX receptor 1A (NMDAR1A). The NMDA receptor contains a second subunit  
 XX selected from the subunits 2A (AAQ79375), 2B (AAQ79377), 2C (AAQ79372)  
 XX and 2D (AAQ79378). The receptor forms part of a family of NMDA receptors  
 XX which have cation-selective channels and bind glutamate and NMDA. The  
 XX NMDAR1A gene was obtained from a cDNA library derived from human  
 XX hippocampal tissue RNA using probes corresponding to sequences in the rat  
 XX NMDAR1A receptor cDNA. 8 clones were isolated. The full length cDNA  
 XX encoding the R1A receptor was generated by ligating the 2.1 kb  
 XX ECORI-HindIII fragment from clone NMDA11 (AAQ79385), containing the 5'  
 XX portion of the gene, with the 3.3 kb BglII-EcoRI fragment of clone NMDA10  
 XX (AAQ79384), containing the 3' portion of the gene. The fragments were  
 XX ligated into the plasmid pcDNA1. The resultant clone NMDAR1A contains 261  
 XX bp of 5' untranslated DNA, the entire coding region for the NMDAR1A  
 XX receptor and 1220 bp of 3' untranslated DNA. Based on the sequence of  
 XX the 8 clones, derived from screening the library, a series of variants

Search completed: November 1, 2001, 16:24:54  
Time: 49 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2001, 16:24:05 ; Search time 14.37 seconds  
(without alignments)  
588.405 Million cell updates/sec

Title: US-09-652-345-6  
Perfect score: 543  
Sequence: 1 IILLVSDHGGRAAKRLET.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	100.0	885	2 JN0339	N-methyl-D-aspartate
2	543	100.0	901	2 JN0337	N-methyl-D-aspartate
3	543	100.0	922	2 JN0338	N-methyl-D-aspartate
4	543	100.0	938	2 S19710	N-methyl-D-aspartate
5	540	99.4	938	2 S21104	N-methyl-D-aspartate
6	538	99.1	938	2 A46612	N-methyl-D-aspartate
7	524	96.5	965	2 I51244	N-methyl-D-aspartate
8	522.5	96.2	906	2 A46296	N-methyl-D-aspartate
9	522.5	96.2	906	2 JN0341	N-methyl-D-aspartate
10	522.5	96.2	922	2 JN0340	N-methyl-D-aspartate
11	522.5	96.2	959	2 JN0336	N-methyl-D-aspartate
12	517.5	95.3	943	2 A47551	N-methyl-D-aspartate
13	184.5	34.0	997	2 S33754	glutamate receptor
14	119	21.9	950	2 T51134	ionotropic glutamate
15	119	21.9	953	2 E84732	probable ligand-gate
16	111.5	20.5	1012	2 T13603	probable N-methyl-
17	107	19.7	941	2 T51135	ligand-gated chann
18	107	19.7	962	2 D86186	hypothetical prote
19	101	18.6	976	2 T51137	ionotropic glutama
20	98	18.0	1039	2 T45779	probable glutamate
21	97.5	18.0	925	2 T51133	ligand gated chann
22	97.5	18.0	951	2 T51132	probable glutamate
23	97.5	18.0	975	2 A84550	probable ligand-ga
24	95.5	17.6	912	2 T51131	ligand gated chann
25	94	17.3	795	2 T20939	hypothetical prote
26	92.5	17.0	1323	2 T178557	N-methyl-D-asparta
27	92.5	17.0	1323	2 S27224	N-methyl-D-asparta
28	90.5	16.7	1356	1 C45219	N-methyl-D-asparta
29	88.5	16.3	920	2 B84640	probable ligand-ga

30	88	16.2	933	2 C96495	probable ligand-ga
31	87	16.0	921	2 T51136	ionotropic glutama
32	87	16.0	923	2 F84732	probable ligand-ga
33	86.5	15.9	925	2 T06128	hypothetical prote
34	81	14.9	723	2 I39066	N-methyl-D-asparta
35	81	14.9	1482	2 B43274	N-methyl-D-asparta
36	81	14.9	1482	2 I49704	glutamate receptor
37	81	14.9	1484	2 S52086	N-methyl-D-asparta
38	78	14.4	1464	1 S29159	glutamate receptor
39	78	14.4	1464	2 A43274	N-methyl-D-asparta
40	78	14.4	1464	2 S47555	N-methyl-D-asparta
41	77.5	14.3	1203	2 I55466	N-methyl-D-asparta
42	77.5	14.3	1239	2 I49705	glutamate receptor
43	76.5	14.1	962	2 C43274	N-methyl-D-asparta
44	76.5	14.1	1250	1 B45219	N-methyl-D-asparta
45	76	14.0	239	2 A83953	uridylate kinase s

## ALIGNMENTS

RESULT 1  
JN0339  
N-methyl-D-aspartate receptor 1 precursor, splice form E - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 15-Sep-2000  
C:Accession: JN0339  
R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.  
Biochem. Biophys. Res. Commun. 185, 826-832, 1992  
A:Title: Structures and properties of seven isoforms of the NMDA receptor generated b  
A:Reference number: JN0336; MUID:92328785  
A:Accession: JN0339  
A:Molecule type: mRNA  
A:Residues: 1-885 <MOR>  
A:Note: neither amino acid nor nucleotide sequence is complete  
C:Comment: This protein plays a key role in memory acquisition, learning and neurolog  
C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.  
C:Superfamily: glutamate receptor; glutamate receptor homology  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-885/Product: N-methyl-D-aspartate receptor 1E #status predicted <MAT>  
F:427-848/Domain: glutamate receptor homology <GRH>  
F:562-580/Domain: transmembrane #status predicted <TM1>  
F:600-620/Domain: transmembrane #status predicted <TM2>  
F:631-649/Domain: transmembrane #status predicted <TM3>  
F:813-833/Domain: transmembrane #status predicted <TM4>  
F:61,203,239,276,300,350,368,440,471,491,875/Binding site: carbohydrate (Asn) (coval  
F:593,676,688,741,766/Binding site: phosphate (Ser) (covalent) #status predicted  
F:683/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 543; DB 2; Length 885;					
Best Local Similarity 100.0%; Pred. No. 4.2e-43;					
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 IILLVSDHGGRAAKRLETLLERESKAEKVLQDFDGTGNTVALLMEARELEARVILS 60					
Db 163 IILLVSDHGGRAAKRLETLLERESKAEKVLQDFDGTGNTVALLMEARELEARVILS 222					
QY 61 ASEDATATVRAAAMLNMTSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111					
Db 223 ASEDATATVRAAAMLNMTSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273					
RESULT 2					
JN0337					
N-methyl-D-aspartate receptor 1 precursor, splice form C - rat					
C:Species: Rattus norvegicus (Norway rat)					
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Sep-2000					
C:Accession: JN0337					
R:Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.					
Biochem. Biophys. Res. Commun. 185, 826-832, 1992					
A:Title: Structures and properties of seven isoforms of the NMDA receptor generated b					

A:Reference number: JN0336; MUID:92328785

A:Accession: JN0337

A:Molecule type: mRNA

A:Residues: 1-901 <MOR>

C:Comment: This protein plays a key role in memory acquisition, learning and neurologic

C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.

C:Superfamily: glutamate receptor; glutamate receptor homology

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein

F:1-901/Product: N-methyl-D-aspartate receptor 1C #status predicted <MAT>

F:427-848/Domain: glutamate receptor homology <GRH>

F:562-580/Domain: transmembrane #status predicted <TM1>

F:600-620/Domain: transmembrane #status predicted <TM2>

F:813-833/Domain: transmembrane #status predicted <TM3>

F:203-239,276,300,350,368,440,471,491/Binding site: carbohydrate (Asn) (covalent) #st

F:676,688,741,766/Binding site: phosphate (Ser) (covalent) #status predicted

F:676,688,741,766/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 543; DB 2; Length 901;

Best Local Similarity 100.0%; Pred. No. 4.3e-43;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 60

DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111

DB 223 ASEDAAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 3

JN0338

N-methyl-D-aspartate receptor 1 precursor, splice form D - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 15-Sep-2000

C:Accession: JN0338

R: Sugihara, H.; Moriyoshi, K.; Ishii, T.; Masu, M.; Nakanishi, S.

Biochem. Biophys. Res. Commun. 185, 826-832, 1992

A:Title: Structures and properties of seven isoforms of the NMDA receptor generated by a

A:Reference number: JN0336; MUID:92328785

A:Accession: JN0338

A:Molecule type: mRNA

A:Residues: 1-922 <MOR>

C:Comment: This protein plays a key role in memory acquisition, learning and neurologic

C:Comment: This protein mediates neuronal functions in glutamate neurotransmission.

C:Superfamily: glutamate receptor; glutamate receptor homology

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; transmembrane protein

F:1-922/Product: N-methyl-D-aspartate receptor 1D #status predicted <MAT>

F:427-848/Domain: glutamate receptor homology <GRH>

F:562-580/Domain: transmembrane #status predicted <TM1>

F:600-620/Domain: transmembrane #status predicted <TM2>

F:813-833/Domain: transmembrane #status predicted <TM3>

F:203-239,276,300,350,368,440,471,491,912/Binding site: carbohydrate (Asn) (covalent)

F:593,676,688,741,766/Binding site: phosphate (Ser) (covalent) #status predicted

F:593,676,688,741,766/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 543; DB 2; Length 922;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 60

DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111

DB 223 ASEDAAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 4

S19710

N-methyl-D-aspartate receptor chain NMDA-R1A (alternatively spliced) - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999

C:Accession: S19710; B46168

R:Moriyoshi, K.; Masu, M.; Ishii, T.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.

Nature 354, 31-37, 1991

A:Title: Molecular cloning and characterization of the rat NMDA receptor.

A:Reference number: S19710; MUID:92049750

A:Accession: S19710

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-938 <MOR>

A:Cross-references: EMBL:X63255; NID:g57847; PIDN:CAA44914.1; PID:g57848

R:Nakanishi, N.; Axel, R.; Shneider, N.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 8552-8556, 1992

A:Title: Alternative splicing generates functionally distinct N-methyl-D-aspartate re

A:Reference number: A46168; MUID:92409554

A:Accession: B46168

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-938 <NAK>

A:Note: sequence extracted from NCBI backbone (NCBIP:113945)

C:Superfamily: glutamate receptor; glutamate receptor homology

C:Keywords: phosphoprotein; transmembrane protein

F:427-848/Domain: glutamate receptor homology <GRH>

Query Match 100.0%; Score 543; DB 2; Length 938;

Best Local Similarity 100.0%; Pred. No. 4.5e-43;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 60

DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111

DB 223 ASEDAAATVYRAAAMNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273

RESULT 5

S21104

N-methyl-D-aspartate receptor zeta-1 chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence\_revision 01-Sep-1995 #text\_change 20-Jun-2000

C:Accession: S21104

R:Yamazaki, M.; Mori, H.; Araki, K.; Mori, K.J.; Mishina, M.

FEBS Lett. 300, 39-45, 1992

A:Title: Cloning, expression and modulation of a mouse NMDA receptor subunit.

A:Reference number: S21104; MUID:92192280

A:Accession: S21104

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-938 <YAM>

A:Cross-references: GB:D10028; NID:g220412; PIDN:BAA00920.1; PID:g220413

C:Superfamily: glutamate receptor; glutamate receptor homology

C:Keywords: phosphoprotein; transmembrane protein

F:427-848/Domain: glutamate receptor homology <GRH>

Query Match 99.4%; Score 540; DB 2; Length 938;

Best Local Similarity 99.1%; Pred. No. 8.6e-43;

Matches 110; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 60

DB 163 IILLVSDHDEGRAAKRLETLLEERESKAQKLVQDPGKNTVALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
|||||  
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 6  
A46612  
N-methyl-D-aspartate receptor chain 1 precursor, splice form 3 - human  
N:Alternate names: N-methyl-D-aspartate glutamate receptor channel; NMDAR1  
N:Contains: N-methyl-D-aspartate receptor 1 precursor splice form 2  
C:Species: Homo sapiens (man)  
C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C:Accession: A46612; A59066; B59066  
R:Karp, S.J.; Masu, M.; Eki, T.; Ozawa, K.; Nakanishi, S.  
J. Biol. Chem. 268, 3728-3733, 1993  
A:Title: Molecular cloning and chromosomal localization of the key subunit of the human  
A:Reference number: A46612; MUID:93155233  
A:Accession: A46612  
A:Molecule type: mRNA  
A:Residues: 1-938 <KAR>  
A:Cross-references: GB:D13515; NID:g219919; PIDN:BAA02732.1; PID:g219920  
A:Experimental source: brain  
A:Note: Sequence extracted from NCBI backbone (NCBIN:124469, NCBIP:124470)  
R:Foldes, R.L.; Rampeasad, V.; Kamboj, R.K.  
Gene 131, 293-298, 1993  
A:Title: Cloning and sequence analysis of cDNAs encoding human hippocampus N-methyl-D-as  
A:Reference number: JN0838; MUID:94010324  
A:Accession: A59066  
A:Molecule type: mRNA  
A:Residues: 300-863, 901-938 <FOLL1>  
A:Cross-references: GB:L13267; NID:g292284; PIDN:AAA36198.1; PID:g292285  
A:Experimental source: hippocampus  
A:Accession: B59066  
A:Molecule type: mRNA  
A:Residues: 11-935, 'T', 937-938 <FOLL2>  
A:Cross-references: GB:L13268; NID:g292286; PIDN:AAB59361.1; PID:g292287  
A:Experimental source: hippocampus  
A:Note: Sequence extracted from GenBank; the codons given for 488-Lys (GAG) and 936-Arg  
C:Comment: This receptor is a member of the family of glutamate-gated ion channels. It i  
e, neuronal degeneration, and neuronal cell death.  
C:Comment: For other alternative splice forms, see PIR:A47551.  
C:Genetics:  
A:Gene: GDB:GRIN1; NMDAR1  
A:Cross-references: GDB:134707; OMIM:138249  
A:Map position: 9q34.3-q34.3  
C:Superfamily: Glutamate receptor; glutamate receptor homology  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; receptor; transmembrane  
F:1-938/Product: N-methyl-D-aspartate receptor 1 precursor splice form 3 #status predict  
F:1-863, 901-938/Product: N-methyl-D-aspartate receptor 1 precursor splice form 3 #status  
F:1-868/Domain: signal sequence #status predicted <Sig>  
F:868-848/Domain: glutamate receptor homology <GRH>  
F:862-580/Domain: transmembrane #status predicted <TRM1>  
F:600-620/Domain: transmembrane #status predicted <TRM2>  
F:631-649/Domain: transmembrane #status predicted <TRM3>  
F:813-833/Domain: transmembrane #status predicted <TRM4>  
F:61,203,239,276,300,350,368,440,471,491,771/Binding site: carbohydrate (Asn) (covalent)  
F:593,687,713/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre  
F:676,741/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predict  
F:681,711/Binding site: phosphate (Tyr) (covalent) #status predicted  
F:683/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:748/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted  
F:766/Binding site: phosphate (Ser) (covalent) (by CAMP- and CGMP-dependent kinases) #st

Query Match 99.1%; Score 538; DB 2; Length 938;  
Best Local Similarity 98.2%; Pred. No. 1.3e-42;  
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IILLVSDHGEHRAAKRLETLLEERESKAEKVLQDPGTKNVTALLMEARELEARVILS 60  
|||||  
Db 163 IILLVSDHGEHRAAKRLETLLEERESKAEKVLQDPGTKNVTALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
|||||  
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 7  
N-methyl-D-aspartate receptor type 1 - duck  
C:Species: Anas platyrhynchos (domestic duck)  
C>Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 20-Jun-2000  
C:Accession: I51244  
R:Kurosawa, N.; Kondo, K.; Kimura, N.; Ikeda, T.; Tsukada, Y.  
Neurochem. Res. 19, 575-580, 1994  
A:Title: Molecular cloning and characterization of avian N-methyl-D-aspartate recepto  
A:Reference number: I51244; MUID:94344315  
A:Accession: I51244  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-965 <KUR>  
A:Cross-references: GB:D83352; NID:g1199922; PIDN:BAA11898.1; PID:g1199923; GB:S71540  
C:Superfamily: glutamate receptor; glutamate receptor homology  
F:427-846/Domain: glutamate receptor homology <GRH>

Query Match 96.5%; Score 524; DB 2; Length 965;  
Best Local Similarity 92.8%; Pred. No. 2.8e-41;  
Matches 103; Conservative 8; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IILLVSDHGEHRAAKRLETLLEERESKAEKVLQDPGTKNVTALLMEARELEARVILS 60  
|||||  
Db 163 IILLVSDHGEHRAAKRLETLLEERESKAEKVLQDPGTKNVTALLMEARELEARVILS 222

QY 61 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111  
|||||  
Db 223 ASEDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 273

RESULT 8  
A46296  
N-methyl-D-aspartate receptor (NMDAR1) splice form NR1b - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Aug-1999  
C:Accession: A46296  
R:Durand, G.M.; Gregor, P.; Zheng, X.; Bennett, M.V.; Uhl, G.R.; Zukin, R.S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 9359-9363, 1992  
A:Title: Cloning of an apparent splice variant of the rat N-methyl-D-aspartate recept  
A:Reference number: A46296; MUID:93028464  
A:Accession: A46296  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-906 <DUR>  
A:Cross-references: GB:S46394; GB:L01632; NID:g257305; PIDN:AAB23610.1; PID:g257306  
A:Experimental source: ventral midbrain  
A:Note: sequence extracted from NCBI backbone (NCBIN:116057, NCBIN:116064, NCBIP:1160  
C:Superfamily: glutamate receptor; glutamate receptor homology  
F:448-869/Domain: glutamate receptor homology <GRH>

Query Match 96.2%; Score 522.5; DB 2; Length 906;  
Best Local Similarity 84.1%; Pred. No. 3.6e-41;  
Matches 111; Conservative 0; Mismatches 0; Indels 21; Gaps 1;  
QY 1 IILLVSDHGEHRAAKRLETLLEERESKAEKVLQDPGTKNVTALLMEARELEARVILS 39  
|||||  
Db 163 IILLVSDHGEHRAAKRLETLLEERESKAEKVLQDPGTKNVTALLMEARELEARVILS 222

QY 40 KNTALLMEARELEARVILSASEDDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRY 99  
|||||  
Db 223 KNTALLMEARELEARVILSASEDDAAATVYRAAAMLNMTGSGYVWLVGEREISGNALRY 282

QY 100 APDGIIGLQLIN 111  
|||||  
Db 283 APDGIIGLQLIN 294



A:Accession: PC4039  
A:Molecule type: DNA  
A:Residues: 1-86 <zim>  
A:Cross-references: EMBL:Z32772; NID:g807892  
A:Note: the authors translated the codon CGC for residue 5 as Ala, TGC for residue 22  
A:Note: this translation is not annotated in GenBank entry HSNMDARIA, release 111.0  
C:Comment: This receptor is a member of the family of glutamate-gated ion channels. I  
e, neuronal degeneration, and neuronal cell death.  
C:Comment: For other alternative splice forms, see PIR:A46612.  
C:Genetics:  
A:Gene: GDB:GRIN1; NMDAR1  
A:Cross-references: GDB:134707; OMIM:138249  
A:Map position: 9q34.3-9q34.3  
C:Superfamily: glutamate receptor; glutamate receptor homology  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; receptor; transmembr  
F:1-190,212-884,922-943/Product: N-methyl-D-aspartate receptor 1 precursor splice for  
F:1-190,212-943/Product: N-methyl-D-aspartate receptor 1 precursor splice form 4 #sta  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-943/Product: N-methyl-D-aspartate receptor 1 #status predicted <MAT>  
F:448-869/Domain: glutamate receptor homology <GRH>  
F:583-601/Domain: transmembrane #status predicted <TRM1>  
F:621-641/Domain: transmembrane #status predicted <TRM2>  
F:652-670/Domain: transmembrane #status predicted <TRM3>  
F:834-854/Domain: transmembrane #status predicted <TRM4>  
F:61,224,260,297,321,371,389,461,492,512,933/Binding site: carbohydrate (Asn) (coval  
F:614,708,734/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status  
F:697,762/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pred  
F:702,732/Binding site: phosphate (Tyr) (covalent) #status predicted  
F:704/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict  
F:769/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict  
F:787/Binding site: phosphate (Ser) (covalent) (by CAMP- and cGMP-dependent kinases)

Query Match 95.3%; Score 517.5; DB 2; Length 943;  
Best Local Similarity 82.8%; Pred. No. 1.1e-40;  
Matches 109; Conservative 2; Mismatches 0; Indels 21; Gaps 1;  
  
QY 1 IILLVSDHDHGRAQKRLTLLERES-----KAEKVLQFDPGT 39  
Db 163 IILLVSDHDHGRAQKRLTLLERESKSKRNYENLDQLSDYDKRGPKAEKVLQFDPGT 222  
  
QY 40 KNVTALLMEARELEARVILISASEDDAATVYRAAAMLNMTGSGVYWLVGEREISGNALRY 99  
Db 223 KNVTALLMEARELEARVILISASEDDAATVYRAAAMLNMTGSGVYWLVGEREISGNALRY 282  
  
QY 100 APDGIIGLQLIN 111  
Db 283 APDGIIGLQLIN 294  
  
RESULT 13  
S33754  
glutamate receptor - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S33754  
P:Uitsch, A.; Schuster, C.M.; Laube, B.; Betz, H.; Schmitt, B.  
FEBS Lett. 324, 171-177, 1993  
A:Title: Glutamate receptors of Drosophila melanogaster. Primary structure of a putat  
A:Reference number: S33754; MUID:93285330  
A:Accession: S33754  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-997 <ULT>  
A:Cross-references: EMBL:X71790; NID:g312197; PIDN:CAA50675.1; PID:g312198  
C:Genetics:  
A:Gene: FlyBase:Nmdar  
A:Cross-references: FlyBase:FBgn0010399  
C:Superfamily: glutamate receptor; glutamate receptor homology  
C:Keywords: neurotransmitter receptor  
F:437-867/Domain: glutamate receptor homology <GRH>

```

Query Match          34.0%; Score 184.5; DB 2; Length 997;
Best-Local Similarity 33.0%; Pred. No. 2e-09;
Matches 38; Conservative 30; Mismatches 38; Indels 9; Gaps 2;

OY      1 ILLVSDDEHGRAAOKRLETLLE-----ERESKAERYLOFPDGTKNVTALIMEARELEA 54
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      126 VITIHSSPTDGRALIGRQTTSQTYDDVDVRAVVELVEPEPKLESTTEHLIDMKTNQ 235
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

OY      55 RYIIISSEDDAATVYRAAAMLNMTGSGYVWLVGEBREISGNALKRYAPDGTIGLOL 109
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      236 RYVLYMAYSTEDAOVIFRDAGEYNMGTGECHWVIVTEQALFSN---NTPDGVGLDOL 287
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 14
T51134
Ionotropic glutamate receptor homolog GLR6 [imported] - Arabidopsis thaliana
Accession: T51134
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 18-Aug-2000
Accession: T51134
R:Daveport, R.J.; Kiegle, E.A.; Tester, M.
submitted to the EMBL Data Library, July 1999
A:Description: A cDNA from Arabidopsis thaliana with similarity to animal ionotropic gluta
A:Reference number: 225307
A:Accession: T51134
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-950 <DAV>
A:Cross-references: EMBL:AF170494; PIDN:AAD50976.1
C:Genetics:
A:Gene: GLR6

OY      1 IILVSDDEHGGAQKRETLLEERESKAERYLOFPDGTKN--VTALLMEARELEARYII 58
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      180 VVAIVPDEYGRNGISVGDALAKRAKISTYKAAPPDADNSSISDLASVNLMSRLTFV 239
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

OY      59 LSASEDDAATVYRAAAMLNMTGSGYVWL 86
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      240 VHVNPDSGLNIFSVAKSLGMMGSGYVWI 267
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

OY      15
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      15
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

Probable ligand-gated ion channel subunit [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Accession: E64732
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffitt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487
A:Accession: E64732
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-953 <STD>
A:Cross-references: GB:AF002093; NID:g3831457; PIDN:AAC69939.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g32390
A:Map position: 2

```

Query Match	21.9%	Score 119;	DB 2;	Length 993;
Best Local Similarity	28.4%	Pred. No. 0.0027;		
Matches	25;	Conservative 17;	Mismatches 44;	Indels 2;
				Gaps 1;
Qy	1	IIIVSDDEHGAAQKRETLLEERESKAETLQDPGK--VALLMEARELEKRVII	58	
	:::			::: :::

Db 183 VVALFVDEYERNRNTSVLGDLLAKRRRAKISYKAFPPGADNSSISDLLASVNLMEHSIFV 242

Qy 59 LSASEDDAATYRAAAMLNMTGSGYVWL 86

Db 243 VHVNPDSGLNIFSVAKSLGMMGSGYVWL 270

Search completed: November 1, 2001, 16:25:15  
Job time: 70 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2001, 16:24:30 ; Search time 21 seconds  
(without alignments)  
699,327 Million cell updates/sec

Title: US-09-652-345-6  
Perfect score: 543  
Sequence: 1 IILLVSDHGGRAAKRLET.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16:  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Hit No.	Score	Query Match	Length	Description
1	543	100.0	938	Q62683 rattus norv
2	539	99.3	243	O19067 sus scrofa
3	524	96.5	965	Q91979 anas platyr
4	522.5	96.2	922	Q62646 rattus norv
5	522.5	96.2	943	Q62648 rattus norv
6	517.5	95.3	906	Q9UPF9 homo sapien
7	517.5	95.3	943	Q9UPF8 homo sapien
8	462.5	85.2	904	Q12868 homo sapien
9	447.5	82.4	195	Q12868 homo sapien
10	415	76.4	966	Q33338 apteronotus
11	184.5	34.0	997	Q24418 drosophila
12	180	33.1	126	Q91804 xenopus lae
13	119	21.9	950	Q9SW97 arabidopsis
14	119	21.9	953	Q9ZV67 arabidopsis
15	111.5	20.5	604	Q9W582 drosophila
16	111.5	20.5	1012	O76903 drosophila
17	107	19.7	941	Q9SWD9 arabidopsis
18	107	19.7	962	O23048 arabidopsis
19	102.5	18.9	1336	O15399 homo sapien

20	98	18.0	1039	10	Q9SD01	Q9s001 arabidopsis
21	97.5	18.0	925	10	O49119	O49119 arabidopsis
22	97.5	18.0	951	10	Q9ZT36	Q9zt36 arabidopsis
23	97.5	18.0	975	10	O22738	O22738 arabidopsis
24	95.5	17.6	912	10	O9SES5	O9ses5 brassica na
25	94	17.3	795	5	Q22063	Q22063 caenorhabdi
26	92.5	17.0	1323	11	Q62645	Q62645 rattus norv
27	92.5	17.0	1323	11	Q63381	Q63381 rattus norv
28	92.5	17.0	1323	11	Q63382	Q63382 rattus norv
29	92.5	17.0	1356	11	Q63729	Q63729 rattus norv
30	88.5	16.3	920	10	Q9SHV1	Q9shv1 arabidopsis
31	87	16.0	921	10	Q9SDQ4	Q9sdq4 arabidopsis
32	87	16.0	923	10	Q9ZV68	Q9zv68 arabidopsis
33	86.5	15.9	925	10	O65498	O65498 arabidopsis
34	86	15.8	867	10	O9LV72	O9lv72 arabidopsis
35	84.5	15.6	860	10	O9FH75	O9fh75 arabidopsis
36	81	14.9	1482	11	Q62684	Q62684 rattus norv
37	81	14.9	1484	4	Q12919	Q12919 homo sapien
38	81	14.9	1484	4	Q13224	Q13224 homo sapien
39	81	14.9	1484	4	Q9UM56	Q9um56 homo sapien
40	79.5	14.6	940	13	O73635	O73635 fugu rubrip
41	78.5	14.5	1236	4	O15398	O15398 homo sapien
42	78	14.4	814	5	O9VEJ2	O9vej2 drosophila
43	78	14.4	1464	4	Q12879	Q12879 homo sapien
44	78	14.4	1464	11	O08948	O08948 rattus norv
45	77.5	14.3	858	10	Q9SRR4	Q9srr4 arabidopsis

ALIGNMENTS

RESULT		1	
Q62683	AC	Q62683	PRELIMINARY; PRT; 938 AA.
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)	
DE	NMDAR1 GLUTAMATE RECEPTOR SUBUNIT.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Sullivan J.M., Traynelis S.F., Chen H., Escobar W., Heinemann S.F.,		
RA	Liption S.A.;		
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; U11418; AAA19659.1; -.		
DR	HSSP; Q05586; 2NRI.		
DR	InterPro; IPR001311; -.		
DR	InterPro; IPR001320; -.		
DR	InterPro; IPR001508; -.		
DR	InterPro; IPR001622; -.		
DR	InterPro; IPR001828; -.		
DR	Pfam; PF00060; lig_chan; 1.		
DR	PRINTS; PR01094; ANF_receptor; 1.		
DR	SMART; SM00177; NMDARECEPTOR.		
SQ	SMART; SM00079; P8Pe; 1.		
SEQUENCE 938 AA; 105568 MW; 3B279C4925AF16DE CRC64;			
Query Match 100.0%; Score 543; DB 11; Length 938;			
Best Local Similarity 100.0%; Pred. No. 2.4e-42;			
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	IILLVSDHGGRAAKRLETLLERESKAEKVLFQDPGCKNVNTALLMEAREARVILS 60	
Db	163	IILLVSDHGGRAAKRLETLLERESKAEKVLFQDPGCKNVNTALLMEAREARVILS 222	
QY	61	ASEDDAATVYRAAAMLNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 111	
Db	223	ASEDDAATVYRAAAMLNMTGSGYVWLVGERISGNALRYAPDGIIGLQLIN 273	



```
RESULT 2
O19067 ID O19067 PRELIMINARY; PRT; 243 AA.
AC O19067:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE N-METHYL-D-ASPARTATE RECEPTOR (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOTHALAMUS;
RQ Matteri R.L.;
RZ Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008560; AAB63295.1; -.
DR InterPro; IPR001828; -.
DR Pfam; PF01094; ANF_receptor; 1.
FT NON_TER 1 243
FT NON_TER 243 243
SQ SEQUENCE 243 AA; 27122 MW; 910EA8342DB06DDF CRC64;

Query Match 99.3%; Score 539; DB 6; Length 243;
Best Local Similarity 99.1%; Pred. No. 1e-42; Indels 0; Gaps 0;
Matches 110; Conservative 1; Mismatches 0;

QY 1 IILLVSDHGGRAAKRLETLLEERESKAEKVLQFDGCTKNVTALLMEARELEARVILS 60
Db 54 IILLVSDHGGRAAKRLETLLEERESKAEKVLQFDGCTKNVTALLMEARELEARVILS 113
QY 61 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 111
Db 114 ASEDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRYAPDGIIGLQLIN 164

RESULT 3
Q91979 ID Q91979 PRELIMINARY; PRT; 965 AA.
AC Q91979;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE N-METHYL-D-ASPARTATE RECEPTOR TYPE1 PRECURSOR.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC Kimura N.;
RQ Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83352; BAA11898.1; -.
DR HSSP; Q05586; 2NR1.
DR InterPro; IPR001311; -.
DR InterPro; IPR001320; -.
DR InterPro; IPR001508; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR001828; -.
DR Pfam; PF00060; lig_chan; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00177; NMDARECEPTOR.
SQ SEQUENCE 922 AA; 103880 MW; 847CEBD410182B5C CRC64;

Query Match 96.2%; Score 522.5; DB 11; Length 922;
Best Local Similarity 84.1%; Pred. No. 1.9e-40;
Matches 111; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 IILLVSDHGGRAAKRLETLLEERESKAEKVLQFDGCTKNVTALLMEARELEARVILS 39
Db 163 IILLVSDHGGRAAKRLETLLEERESKAEKVLQFDGCTKNVTALLMEARELEARVILS 222
QY 40 KNTVALLMEARELEARVILSASEDDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRY 99
Db 223 KNTVALLMEARELEARVILSASEDDAAATVYRAAAMNMTGSGYVWLVGEREISGNALRY 282
QY 100 APDGIIGLQLIN 111
```

Db 283 APDGIIGLQLIN 294

## RESULT 5

Q62648 ID Q62648 PRELIMINARY; PRT; 943 AA.  
AC Q62648;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE N-METHYL-D-ASPARTATE RECEPTOR NMDAR1-3B SUBUNIT.  
GN NMDAR1.

OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=FOREBRAIN;

RX MEDLINE=93264089; PubMed=7684237;

RA Hollmann M., Boulter J., Maron C., Beasley L., Sullivan J., Pecht G.,  
Heinemann S.;

"zinc potentiates agonist-induced currents at certain splice variants  
of the NMDA receptor.";  
RL Neuron 10:943-954(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=FOREBRAIN;

RA Boulter J.;

RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; U08266; AAB50931.1; -.

DR HSSP; Q05586; 2NRI.

DR InterPro; IPR001311; -.

DR InterPro; IPR001320; -.

DR InterPro; IPR001508; -.

DR InterPro; IPR001622; -.

DR InterPro; IPR001828; -.

DR Pfam; PF00060; lig\_chan; 1.

DR Pfam; PF01094; ANF\_receptor; 1.

DR PRINTS; PR00177; NMDARECEPTOR.

DR SMART; SM00079; PBPe; 1.

SQ SEQUENCE 943 AA; 106150 MW; 3D521E349A5741BB CRC64;

## Query Match

Best Local Similarity 96.2%; Score 522.5; DB 11; Length 943;

Matches 111; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 IILLVSDHDEGAAQKRLETLLEERES-----KAEKVLQFDPGT 39  
|||||  
163 IILLVSDHDEGAAQKRLETLLEERESKKNRYENLDQLSYDNKRGPKAEKVLQFDPGT 222

QY 40 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 99  
|||||  
223 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 282

Db 100 APDGIIGLQLIN 111

Db 283 APDGIIGLQLIN 294

## RESULT 6

Q9UPF9 ID Q9UPF9 PRELIMINARY; PRT; 906 AA.

AC Q9UPF9;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE NMDAR1 SUBUNIT ISOFORM 3B.

GN HNMAR1-3B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97375389; PubMed=9231706;

RA Nash N.R., Hellman C.J., Rees H.D., Levey A.I.;

"Cloning and localization of exon 5-containing isoforms of the NMDAR1  
subunit in human and rat brains.";

RL J. Neurochem. 69:485-493(1997).

DR EMBL; AF015730; AAB67723.1; -.

DR HSSP; Q05586; 2NRI.

DR InterPro; IPR001311; -.

DR InterPro; IPR001320; -.

DR InterPro; IPR001508; -.

DR InterPro; IPR001622; -.

DR InterPro; IPR001828; -.

DR Pfam; PF00060; lig\_chan; 1.

DR Pfam; PF01094; ANF\_receptor; 3.

DR PRINTS; PR00177; NMDARECEPTOR.

DR SMART; SM00079; PBPe; 1.

SQ SEQUENCE 906 AA; 101884 MW; 76199662AE0F313A CRC64;

## Query Match

Best Local Similarity 82.6%; Score 517.5; DB 4; Length 906;

Matches 109; Conservative 2; Mismatches 0; Indels 21; Gaps 1;

QY 1 IILLVSDHDEGAAQKRLETLLEERES-----KAEKVLQFDPGT 39  
|||||  
163 IILLVSDHDEGAAQKRLETLLEERESKKNRYENLDQLSYDNKRGPKAEKVLQFDPGT 222

QY 40 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 99  
|||||  
223 KNTVALLMEARELEARVILSASEDDAATVYRAAAMLNTGSGYVWLVGEREISGNALRY 282

QY 100 APDGIIGLQLIN 111

Db 283 APDGIIGLQLIN 294

## RESULT 7

Q9UPF8

ID Q9UPF8 PRELIMINARY; PRT; 943 AA.

AC Q9UPF8;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE NMDAR1 SUBUNIT ISOFORM 4B.

GN HNMAR1-4B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97375389; PubMed=9231706;

RA Nash N.R., Hellman C.J., Rees H.D., Levey A.I.;

"Cloning and localization of exon 5-containing isoforms of the NMDAR1  
subunit in human and rat brains.";

RL J. Neurochem. 69:485-493(1997).

DR EMBL; AF015731; AAB67724.1; -.

DR HSSP; Q05586; 2NRI.

DR InterPro; IPR001311; -.

DR InterPro; IPR001320; -.

DR InterPro; IPR001508; -.

DR InterPro; IPR001622; -.

DR InterPro; IPR001828; -.

DR Pfam; PF00060; lig\_chan; 1.

DR Pfam; PF01094; ANF\_receptor; 3.

DR PRINTS; PR00177; NMDARECEPTOR.

DR SMART; SM00079; PBPe; 1.

SQ SEQUENCE 943 AA; 106048 MW; 90905DD81BE7FE69 CRC64;

Query Match					
Best Local Similarity 95.3%; Score 517.5; DB 4; Length 943;					
Matches 109; Conservative 2; Mismatches 0; Indels 21; Gaps					
QY	1	IILLVSDDHGEGRAAQKRLFTLLERES-----KAENVLQDPGT 39			
Dd	163	IILLVSDDHGEGRAAQKRLFTLLERESKKRNYENLDQLSYDNKRGPRAEKVLQDPGT 222			
QY	40	KNTALLMEARELEARVIILTSASEDDAAATVYRAAAMNMTGSGYWLVGERETSGNALRY 99			
Dd	223	KNTALLMEAKELEARVIILTSASEDDADTAATVYRAAAMNMTGSGYWLVGERETSGNALRY 282			
QY	100	APDGIIIGLQLIN I11			
Dd	283	APDGIIGLQLIN 294			
R	ALT	8			
ID	Q91977	PRELIMINARY; PRT; 904 AA.			
AC	Q91977; Q91805;				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DE	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)				
DE	NMDA GLUTAMATE RECEPTOR SUBUNIT PRECURSOR (NMDA RECEPTOR).				
GN	NR1.				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
TX	TISSUE-BRAIN:				
RC	MEDLINE=97115781; PubMed=8955083;				
RA	Soloviev M.M., Brierley M.J., Shao Z.Y., Mellor I.R., Volkova T.M.,				
RA	Kamboj R., Ishimaru H., Sudan H., Harris J., Foldes R.L.,				
RA	Grishin E.V., Usherwood P.N.R., Barnard E.A.;				
RT	"Functional expression of a recombinant unitary glutamate receptor				
RT	from Xenopus, which contains N-methyl-D-aspartate (NMDA) and non-NMDA				
RT	receptor subunits.";				
J	J. Biol. Chem. 271:32572-32579(1996).				
RN	[2]				
REMARKS	SEQUENCE OF 79-225 FROM N.A.				
TISSUE-BRAIN:					
SOL	Soloviev M.M.;				
RL	Submitted (Aug-1996) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; X94156; CAA63871.1; -				
DR	EMBL; X94081; CAA63825.1; -				
DR	EMBL; X99885; CAA68167.1; -				
DR	HSP; Q05586; 2NR1.				
DR	InterPro; IPRO01311; -				
DR	InterPro; IPRO01320; -				
DR	InterPro; IPRO01508; -				
DR	InterPro; IPRO01622; -				
DR	InterPro; IPRO01828; -				
DR	Pfam; PF00060; lig_chan.1.				
DR	Pfam; PF01094; ANF_receptor.1.				
DR	SMART; PR00177; NMDARECEPTOR.				
DR	SNP; SNM0079; PBPe; 1.				
KW	Signal.				
FT	SIGNAL				
FT CHAIN	21 904				
FT SIGNAL	1 20				
FT POTENTIAL	POTENTIAL.				
SEQUENCE	904 AA; 101893 MW; 46D8FE0EA6D903F2 CRC64;				
Query Match					
Best Local Similarity 85.2%; Score 462.5; DB 13; Length 904;					
Matches 94; Conservative 14; Mismatches 3; Indels 21; Gaps					
QY	1	IILLVSDHHEGRAAKRLETLLERES-----KAENVLQDPGT 39			
Dd	1	IILLVSDHHEGRAAKRLETLLERES-----KAENVLQDPGT 39			



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ID Q91804 PRELIMINARY; PRT; 126 AA.
AC Q91804;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE NMDA RECEPTOR (FRAGMENT).
GN NRY.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Soloviev M.M.;
RA Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
EMBL: X98884; CAA68166.1; -.
DR InterPro: IPR001828; -.
DR Pfam: PF01094; ANF_receptor; 1.
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 14309 MW; 7E170188153EDC4F CRC64;

Query Match 33.1%; Score 180; DB 13; Length 126;
Best Local Similarity 81.0%; Pred. No. 1.4e-09;
Matches 34; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 IILLVSDHGGRAQKRLTLLERESKAQKVLQFDPTGNV 42
DB 85 VILLVSDHGGRAQKRLTLLERESKAQKVLQFDPTGNL 126

RESULT 13
Q9SW97 PRELIMINARY; PRT; 950 AA.
AC Q9SW97;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE IONOTROPIC GLUTAMATE RECEPTOR ORTHOLOG GLR6.
GN GLR6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE SEEDLING;
RA Davenport R.J., Kiegle E.A., Tester M.;
RA "A cDNA from Arabidopsis thaliana with similarity to animal ionotropic
RT glutamate receptors."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF170494; AAD50976.1; -.
DR InterPro: IPR001311; -.
DR InterPro: IPR001320; -.
DR InterPro: IPR001828; -.
DR InterPro: IPR002048; -.
DR Pfam: PF00060; lig_chan; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
DR SMART: SM00079; PBPe; 1.
KW Receptor.
SQ SEQUENCE 950 AA; 106437 MW; 6563AE3C74D55C7D CRC64;

Query Match 21.9%; Score 119; DB 10; Length 950;
Best Local Similarity 28.4%; Pred. No. 0.009;
Matches 25; Conservative 17; Mismatches 44; Indels 2; Gaps 1;

QY 1 IILLVSDHGGRAQKRLTLLERESKAQKVLQFDPTGN--VTALLMEARELEARVII 58
DB 183 VVAFVDDDEYGRNGISVLGDALAKKRAKISYKAAFPFGADNSSISDLLASVNLMSRIFV 242

Query Match 21.9%; Score 119; DB 10; Length 953;
Best Local Similarity 28.4%; Pred. No. 0.0091;
Matches 25; Conservative 17; Mismatches 44; Indels 2; Gaps 1;

QY 1 IILLVSDHGGRAQKRLTLLERESKAQKVLQFDPTGN--VTALLMEARELEARVII 58
DB 183 VVAFVDDDEYGRNGISVLGDALAKKRAKISYKAAFPFGADNSSISDLLASVNLMSRIFV 242
QY 59 LSASEDDRAATVYRAAAMLNMTGSGYVWL 86
DB 243 VHVNPDSGLNIFSVAKSLGMMGSGYVWI 270

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DB 180 VVAFVDDDEYGRNGISVLGDALAKKRAKISYKAAFPFGADNSSISDLLASVNLMSRIFV 239
QY 59 LSASEDDRAATVYRAAAMLNMTGSGYVWL 86
DB 240 VHVNPDSGLNIFSVAKSLGMMGSGYVWI 267

RESULT 14
Q9ZV67 PRELIMINARY; PRT; 953 AA.
AC Q9ZV67;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PUTATIVE ION CHANNEL PROTEIN.
GN T32F6.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Rønning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RA "Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC005700; AAC69939.1; -.
DR InterPro: IPR001311; -.
DR InterPro: IPR001320; -.
DR Pfam: PF00060; lig_chan; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR SMART: SM00079; PBPe; 1.
SQ SEQUENCE 953 AA; 106810 MW; 9C13F10ECFF5116 CRC64;

Query Match 21.9%; Score 119; DB 10; Length 953;
Best Local Similarity 28.4%; Pred. No. 0.0091;
Matches 25; Conservative 17; Mismatches 44; Indels 2; Gaps 1;

QY 1 IILLVSDHGGRAQKRLTLLERESKAQKVLQFDPTGN--VTALLMEARELEARVII 58
DB 183 VVAFVDDDEYGRNGISVLGDALAKKRAKISYKAAFPFGADNSSISDLLASVNLMSRIFV 242
QY 59 LSASEDDRAATVYRAAAMLNMTGSGYVWL 86
DB 243 VHVNPDSGLNIFSVAKSLGMMGSGYVWI 270

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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Borkan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RA "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
DR EMBL; AE003421; AAP45639.1; -.  
DR HSSP; P19491; IGR2.  
DR FlyBase; FBgn0014432; EG:80H7.7.  
DR InterPro; IPR001311; -.  
DR Pfam; PF01094; ANF\_receptor; 1.  
SQ SEQUENCE 604 AA; 67462 MW; FB4DFBCDA10D9E49 CRC64;

Query Match 20.5%; Score 111.5; DB 5; Length 604;  
Best Local Similarity 39.4%; Pred. No. 0.025;  
Matches 26; Conservative 15; Mismatches 24; Indels 1; Gaps 1;

QY 43 TALLMEARELEARVILLISASEDDAATVYRAAAMLNMTGSGYVWLGEREI-SGNALRYAP 101  
|: ||| ||||| : : : ||| : : ||| ||| : : |  
115 TSDLMELVNSEARVLLYATQTETILRAAEEMKLTGENTYVWVYSQSVIEKKDAHSQFP 174

QY 102 DGIIGL 107  
|: :|

Db 175 VCMGV 180  
|: :|

Search completed: November 1, 2001, 16:27:36  
Job time: 186 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2001, 16:25:00 ; Search time 11.56 seconds  
(without alignments)  
328.924 Million cell updates/sec

Title: US-09-652-345-6  
Perfect score: 543  
Sequence: 1 IILVSDDEHRAAQRLET.....ISGNALRYAPDGIIGLQLIN 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	100.0	938	1	NMZ1_RAT
2	540	99.4	938	1	NMZ1_MOUSE
3	538	99.1	938	1	NMZ1_HUMAN
4	92.5	17.0	1323	1	NME2_MOUSE
5	81	14.9	1482	1	NME2_MOUSE
6	81	14.9	1482	1	NME2_MOUSE
7	78.5	14.5	1233	1	NME3_HUMAN
8	78	14.4	1464	1	NME1_MOUSE
9	78	14.4	1464	1	NME1_MOUSE
10	77.5	14.3	1237	1	NME3_MOUSE
11	77.5	14.3	1239	1	NME3_MOUSE
12	75	13.8	956	1	GLK4_MOUSE
13	73.5	13.5	866	1	MYSP_SCHJA
14	72.5	13.4	240	1	PYRH_BACSU
15	72.5	13.4	1085	1	CASR_BOVIN
16	72	13.3	956	1	GLK4_HUMAN
17	70.5	13.0	321	1	RT01_YEAST
18	70.5	13.0	496	1	GTR3_CHICK
19	70.5	13.0	908	1	MGR8_HUMAN
20	70.5	13.0	908	1	MGR8_MOUSE
21	70	12.9	877	1	MGR6_HUMAN
22	69.5	12.8	344	1	STSY_RAUSE
23	69.5	12.8	908	1	MGR8_MOUSE
24	69	12.7	912	1	MGR4_HUMAN
25	69	12.7	979	1	GLK5_MOUSE
26	69	12.7	979	1	GLK5_MOUSE
27	68.5	12.6	507	1	PDI_DATGL
28	68.5	12.6	1078	1	CASR_HUMAN
29	68.5	12.6	1079	1	CASR_MOUSE
30	68.5	12.6	1079	1	CASR_MOUSE
31	68	12.5	836	1	GLK1_MOUSE
32	68	12.5	889	1	GLK2_MOUSE
33	68	12.5	908	1	GLK2_HUMAN

34	68	12.5	908	1	GLK2_RAT
35	68	12.5	918	1	GLK1_HUMAN
36	68	12.5	980	1	GLK5_HUMAN
37	67	12.3	417	1	PKRB_LEIME
38	67	12.3	499	1	XYLB_BACSU
39	67	12.3	866	1	MYSP_SCHMA
40	67	12.3	912	1	MGR4_RAT
41	67	12.3	2017	1	MYSN_DROME
42	66.5	12.2	458	1	CD4_MACFA
43	66.5	12.2	458	1	CD4_MACFU
44	66.5	12.2	458	1	CD4_MACMU
45	66.5	12.2	458	1	CD4_MACNE

## ALIGNMENTS

RESULT	1
NMZ1_RAT	
ID	NMZ1_RAT
AC	P35439; STANDARD; PRT; 938 AA.
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	GLUTAMATE [NMDA] RECEPTOR SUBUNIT ZETA 1 PRECURSOR (NR1) (NMD-R1)
DE	(N-METHYL-D-ASPARTATE RECEPTOR).
GN	GRIN1 OR NMDAR1.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=92049750; PubMed=1834949;
RA	Moriyoshi K., Masu M., Ishii T., Shigemoto R., Mizuno N.,
RA	Nakanishi S.;
RT	"Molecular cloning and characterization of the rat NMDA receptor.";
RL	Nature 354:31-37(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92409554; PubMed=1388270;
RA	Nakanishi N., Axel R., Shneider N.A.;
RT	"Alternative splicing generates functionally distinct N-methyl-D-
RT	aspartate receptors.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:8552-8556(1992).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Forebrain;
RX	MEDLINE=93264089; PubMed=7684237;
RA	Hollmann M., Boulter J., Maron C., Beasley L., Sullivan J., Pecht G.,
RA	Heinemann S.;
RT	"Zinc potentiates agonist-induced currents at certain splice variants
RT	of the NMDA receptor.";
RL	Neuron 10:943-954(1993).
RN	[4]
RP	SEQUENCE OF 1-86 FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX	MEDLINE=94002162; PubMed=8399301;
RA	Bai G., Kusia J.W.;
RT	"Cloning and analysis of the 5' flanking sequence of the rat
RT	N-methyl-D-aspartate receptor 1 (NMDAR1) gene.";
RL	Biochim. Biophys. Acta 1152:197-200(1993).
RN	[5]
RP	ALTERNATIVE SPLICING.
RC	TISSUE=Brain;
RX	MEDLINE=92328785; PubMed=1352681;
RA	Sugihara H., Moriyoshi K., Ishii T., Masu M., Nakanishi S.;
RT	"Structures and properties of seven isoforms of the NMDA receptor
RT	generated by alternative splicing.";
RL	Biochem. Biophys. Res. Commun. 185:826-832(1992).
RN	[6]
RP	ALTERNATIVE SPLICING.

RC TISSUE=Brain;  
RX MEDLINE=92339518; PubMed=1386026;  
RA Anantharam V., Panchal R., Wilson A., Koltchin V.V.,  
RT Treisman S.N., Bayley H.;  
RT "Combinatorial RNA splicing alters the surface charge on the NMDA  
RT receptor";  
RL FEBS Lett. 305:27-30(1992).  
CC -!- FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS  
CC POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT  
CC SENSITIVITY TO MAGNESIUM AND IS MODULATED BY GLYCINE. THIS PROTEIN  
CC PLAYS A KEY ROLE IN SYNAPTIC PLASTICITY, SYNAPTOGENESIS,  
CC EXCITOTOXICITY, MEMORY ACQUISITION AND LEARNING. IT MEDIATES  
CC NEURONAL FUNCTIONS IN GLUTAMATE NEUROTRANSMISSION.  
CC -!- SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZETA SUBUNIT.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- ALTERNATIVE PRODUCTS: 7 ISOFORMS; A (SHOWN HERE), B, C, D, E, F  
CC AND G: ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -!- PTM: NMDA IS PROBABLY REGULATED BY C-TERMINAL PHOSPHORYLATION OF  
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CC EMBL: J03875; J03875.  
CC EMBL: J03876; J03876.  
CC EMBL: J03877; J03877.  
CC EMBL: J03878; J03878.  
CC EMBL: J03879; J03879.  
CC EMBL: J03880; J03880.  
CC EMBL: J03881; J03881.  
CC EMBL: J03882; J03882.  
CC EMBL: J03883; J03883.  
CC EMBL: J03884; J03884.  
CC EMBL: J03885; J03885.  
CC EMBL: J03886; J03886.  
CC EMBL: J03887; J03887.  
CC EMBL: J03888; J03888.  
CC EMBL: J03889; J03889.  
CC EMBL: J03890; J03890.  
CC EMBL: J03891; J03891.  
CC EMBL: J03892; J03892.  
CC EMBL: J03893; J03893.  
CC EMBL: J03894; J03894.  
CC EMBL: J03895; J03895.  
CC EMBL: J03896; J03896.  
CC EMBL: J03897; J03897.  
CC EMBL: J03898; J03898.  
CC EMBL: J03899; J03899.  
CC EMBL: J03900; J03900.  
CC EMB







[illegible]

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MEDLINE=92244361; PubMed=13741164;
RA Yaguro H., Mori H., Araki K., Kushiya E., Kutsumada T., Mishina M.;
RA Meguro K., Kumanishi T., Arakawa M., Sakimura K., Mishina M.;
RT "Functional characterization of a heteromeric NMDA receptor channel
RT expressed from cloned cDNAs.";
RL Nature 357:70-74(1992).
CC -1- FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS
CC POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT
CC SENSITIVITY TO MAGNESIUM AND IS MEDIATED BY GLYCINE.
CC -1- SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZETA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
CC EMBL; D10217; BAA01069.1; -.
CC PIR; S29159; S29159.
CC MGD; MGI:95820; Grin2a.
CC InterPro; IPR001320; -.
CC Pfam; PF00060; lig_chan; 1.
CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
CC Transmembrane; Calcium; Magnesium.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 1464 GLUTAMATE [NMDA] RECEPTOR SUBUNIT
CC EPSILON 1.
CC DOMAIN 23 556 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 557 576 1 (POTENTIAL).
CC TRANSMEM 599 619 2 (POTENTIAL).
CC TRANSMEM 629 654 3 (POTENTIAL).
CC TRANSMEM 817 837 4 (POTENTIAL).
CC SITE 614 614 FUNCTIONAL DETERMINANT OF NMDA
CC RECEPTORS (BY SIMILARITY).
CC CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 380 380 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 443 443 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 444 444 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 541 541 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 1464 AA; 165490 MW; 422CD89C56379047 CRC64;
SQ
Query Match 14.4%; Score 78; DB 1; Length 1464;
Best Local Similarity 28.1%; Pred. No. 12;
Matches 18; Conservative 17; Mismatches 25; Indels 4; Gaps 2;

QY 47 MEARELEARVILSASEDDAAVTYRAAANMTGSGYVWLVGEREISGNA---LRYPDG 103
   : : : ||| :|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 217 VLKAKHSSVLLCYSKDEAVLLSEARSGLTGDFWIVPSLV-SVGNTELIPKEFPG 275

QY 104 IIGL 107
   :| :
Db 276 LISV 279

RESULT 9
NMEL_RAT ID NMEL_RAT STANDARD; PRT; 1464 AA.
AC Q00959;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR (N-METHYL
DE D-ASPARTATE RECEPTOR SUBTYPE 2A) (NR2A) (NMDAR2A).
GN GRIN2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
```



RESULT 11

ID	NME3_MOUSE	STANDARD;	PRT;	1239 AA.
AC	Q01098;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C).			
DE	GRIN2C.			
GN				
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=92310564; PubMed=1377365;			
RP	Kutsuwada T., Kashiwabuchi N., Mori H., Sakimura K., Kushiya E., Araki K., Meguro H., Masaki H., Kumanishi T., Arakawa M., Mishina M.,			
RA	"Molecular diversity of the NMDA receptor channel."			
RT	Nature 358:36-41(1992).			
RL	[2]			
RN				
RP	REVISIONS.			
RA	Kashiwabuchi N.;			
RA	Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.			
RL	-!- FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT SENSITIVITY TO MAGNESIUM AND IS MEDIATED BY GLYCINE.			
CC	-!- SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT AND A ZETA SUBUNIT.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.			
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CC	-----			
EMBL;	D10694; BAA01536.1; -			
DR	MGD; MGI:95822; Grin2c.			
DR	InterPro; IPR001320; -			
DR	Pfam; PF00060; lig_chan; 1.			
DR	Receptor; Signal; Transmembrane; Postsynaptic membrane; Calcium; Ionic channel; Magnesium.			
FT	SIGNAL 1 19 POTENTIAL.			
FT	CHAIN 20 1239 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3.			
FT	DOMAIN 20 553 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 554 574 1 (POTENTIAL).			
FT	TRANSMEM 597 617 2 (POTENTIAL).			
FT	TRANSMEM 627 647 3 (POTENTIAL).			
FT	TRANSMEM 815 835 4 (POTENTIAL).			
FT	SITE 612 612 FUNCTIONAL DETERMINANT OF NMDA RECEPTORS (BY SIMILARITY).			
FT	CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 539 539 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	SEQUENCE 1239 AA; 135420 MW; 793E8E731E20C3C9 CRC64;			

Query Match 14.3%; Score 77.5; DB 1; Length 1239;  
 Best Local Similarity 32.1%; Pred. No. 11;  
 Matches 18; Conservative 13; Mismatches 22; Indels 3; Gaps 2;

QY 33 LQDPGKTNV-TALLMEARELVARVILSASEDDAATVYRAAAMLNWTGSGYVWLV 87  
 201 LEIGPGGPRARTQLG--ROVDAPVLVAYCSREAEVLFFAEAQAQGLVGPQHWLV 254

Db

```
FT CARBOHYD 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 539 S -> F (IN REF. 2).
SQ SEQUENCE 956 AA; 107223 MW; 970C9D72C8D74700 CRC64;

Query Match 13.8%; Score 75; DB 1; Length 956;
Best Local Similarity 25.0%; Pred. No. 15;
Matches 25; Conservative 21; Mismatches 48; Indels 6; Gaps 2;

QY 15 QKRLETLLEERESKAQVLPDGTGKNTALLMEARELEARVILSASEDDAATVYRAA 74
Db 176 EKLRLQFLSKDTLSVRMLD---DTRDPTLLKEIRDDKTATIIHANASMSHTILLKAA 232
QY 75 MLNMTGSGYVWLVEREISGNALRYAPD---GIIGLQLIN 111
Db 233 ELGMVSAYTYVFTNLEFSLQRMDSLVDVRNVLGFSIFN 272

RESULT 13
SCHJA
MYSP SCHJA STANDARD; PRT; 866 AA.
AC Q05870: Q26510; Q26518;
DT 01-JUN-1994 (Rel. 29, Created)
DT 13-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PARAMYOSIN (ANTIGEN SJ97).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE;
RX MEDLINE=95407380; PubMed=7676905;
RA Becker M.M., Kalina B.H., Wang W., Harrop S.A., Scott J.C.,
RA Weine G.J., Kurtis J.D., McManus D.P.;
RT "Gene cloning and complete nucleotide sequence of Philippine
RT Schistosoma japonicum paramyosin."
RL Acta Trop. 59:143-147(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JAPANESE;
RX MEDLINE=95034466; PubMed=7947464;
RA Nara T., Matsumoto N., Janecharut T., Matsuda H., Yamamoto K.,
RA Iimura T., Nakamura K.I., Aikawa M., Oswald I., Sher A., Kita K.,
RA Kojima S.;
RT "Demonstration of the target molecule of a protective IgE antibody in
RL secretory glands of Schistosoma japonicum larvae."
RN [3]
RP SEQUENCE OF 171-559 FROM N.A.
RX MEDLINE=93138870; PubMed=1487380;
RA Yang W., Waite G.J., Sculley D.G., Liu X., McManus D.P.;
RT "Cloning and partial nucleotide sequence of Schistosoma japonicum
RT paramyosin: a potential vaccine candidate against schistosomiasis."
RL Int. J. Parasitol. 22:1187-1191(1992).
CC -1- FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF
CC MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.
CC -1- DEVELOPMENTAL STAGE: MAY BE INCORPORATED INTO THE TEGUMENT DURING
CC THE DEVELOPMENT OF SCHISTOSOMULA, THUS BECOMING A TARGET FOR
CC PROTECTIVE IMMUNITY DURING THE MIGRATORY PHASE OF THE PARASITE.
CC -1- SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
CC
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-----
EMBL: Z99112; CAB13524.1; -
DR Subtilist; BG12675; pyrH.
DR Pfam; PF00696; askinase; 1.
KW Transferrase; Kinase; Pyrimidine biosynthesis.
SQ SEQUENCE 240 AA; 25991 MW; 5D9DEF9AA36A29A9 CRC64;
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EMBL: U11825; AAA81003.1; -
DR EMBL; D28811; BAA05972.1; -
DR EMBL; M90492; -; NOT_ANNOTATED_CDS.
DR InterPro; IPR002928; -
DR Pfam; PF01576; Myosin_tail; 1.
KW Coiled coil; Heptad repeat pattern; Muscle protein; Thick filament;
KW Myosin; Antigen.
FT DOMAIN 1 22 NONHELICAL REGION (POTENTIAL).
FT DOMAIN 23 839 COILED COIL (POTENTIAL).
FT DOMAIN 840 866 NONHELICAL REGION (POTENTIAL).
FT DISULFID 750 750 INTERCHAIN (POTENTIAL).
FT CONFLICT 371 371 E -> D (IN REF. 1).
FT CONFLICT 559 559 E -> K (IN REF. 3).
SQ SEQUENCE 866 AA; 100541 MW; 37D7BDF2CF32775D CRC64;

Query Match 13.5%; Score 73.5; DB 1; Length 866;
Best Local Similarity 30.4%; Pred. No. 18;
Matches 24; Conservative 13; Mismatches 29; Indels 13; Gaps 2;

QY 2 ILLVSDHCEGAAQKRLTEL-----LEERESKAQVLPDGTGKNTALLMEARELEA 54
Db 596 IQLANEVEELSRAMENLERLKHAELEETEQRVSEL-----TIQVNTLSNKKRLEG 649
QY 55 RVILLSASEDDAATVYRAA 73
Db 650 DIGVMQADMDDAINKQAA 668

RESULT 14
PYRH_BACSU STANDARD; PRT; 240 AA.
ID PYRH_BACSU STANDARD; PRT; 240 AA.
AC Q31749;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE URIDYLATE KINASE (EC 2.7.4.-) (UK) (URIDINE MONOPHOSPHATE KINASE)
DE (UMP KINASE).
GN PYRH OR SMBA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: URIDINE MONOPHOSPHATE KINASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.
CC -1- SIMILARITY: TO OTHER UMP KINASE; SOME, TO ASPARTOKINASES AND TO
CC GLUTAMATE KINASES.
CC
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-----
EMBL: Z99112; CAB13524.1; -
DR Subtilist; BG12675; pyrH.
DR Pfam; PF00696; askinase; 1.
KW Transferrase; Kinase; Pyrimidine biosynthesis.
SQ SEQUENCE 240 AA; 25991 MW; 5D9DEF9AA36A29A9 CRC64;

Query Match 13.4%; Score 72.5; DB 1; Length 240;
```



FT	TRANSMEM	683	701	III (POTENTIAL).
FT	DOMAIN	702	725	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	726	746	IV (POTENTIAL).
FT	DOMAIN	747	770	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	771	793	V (POTENTIAL).
FT	DOMAIN	794	806	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	807	829	VI (POTENTIAL).
FT	DOMAIN	830	837	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	838	863	VII (POTENTIAL).
FT	DOMAIN	864	1085	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	131	131	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	262	262	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	288	288	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	401	401	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	447	447	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	469	469	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	542	542	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	595	595	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	1085 AA;	121170 MW; 5D66DE8C9CD13E47 CRC64;	
 Query Match                    13.4%; Score 72.5; DB 1; Length 1085;				
Best Local Similarity       23.6%; Pred. No. 29;				
Matches     29; Conservative   18; Mismatches   47; Indels     29; Gaps				
QY	4	LVSDDHGEAAQRKRLTLLERE-----SKAEKVLFQDPGTKNVTALLMEARE 51	:	: :    :
Db	213	IADDDYGRPGIEKFREAEERDICDFSELISQYSDEEKIQOVVEIQNST----- 264	:	: :    :
QY	52	LEARVILSASEDAATVYRAAAMLNMTSGYVWLVGEREISGNALR-----YAPDGIG 106	:	: :    :
Db	265	--AKVIVFSSGGPDLEPLIKEIYVRNITGR--IWLASEAWASSSLAMPEYFHVWGTTG 320	:	: :    :
QY	107	LQL 109	:	: :    :
Db	321	FGL 323	:	: :    :

Search completed: November 1, 2001, 16:27:54  
Job time: 174 sec



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